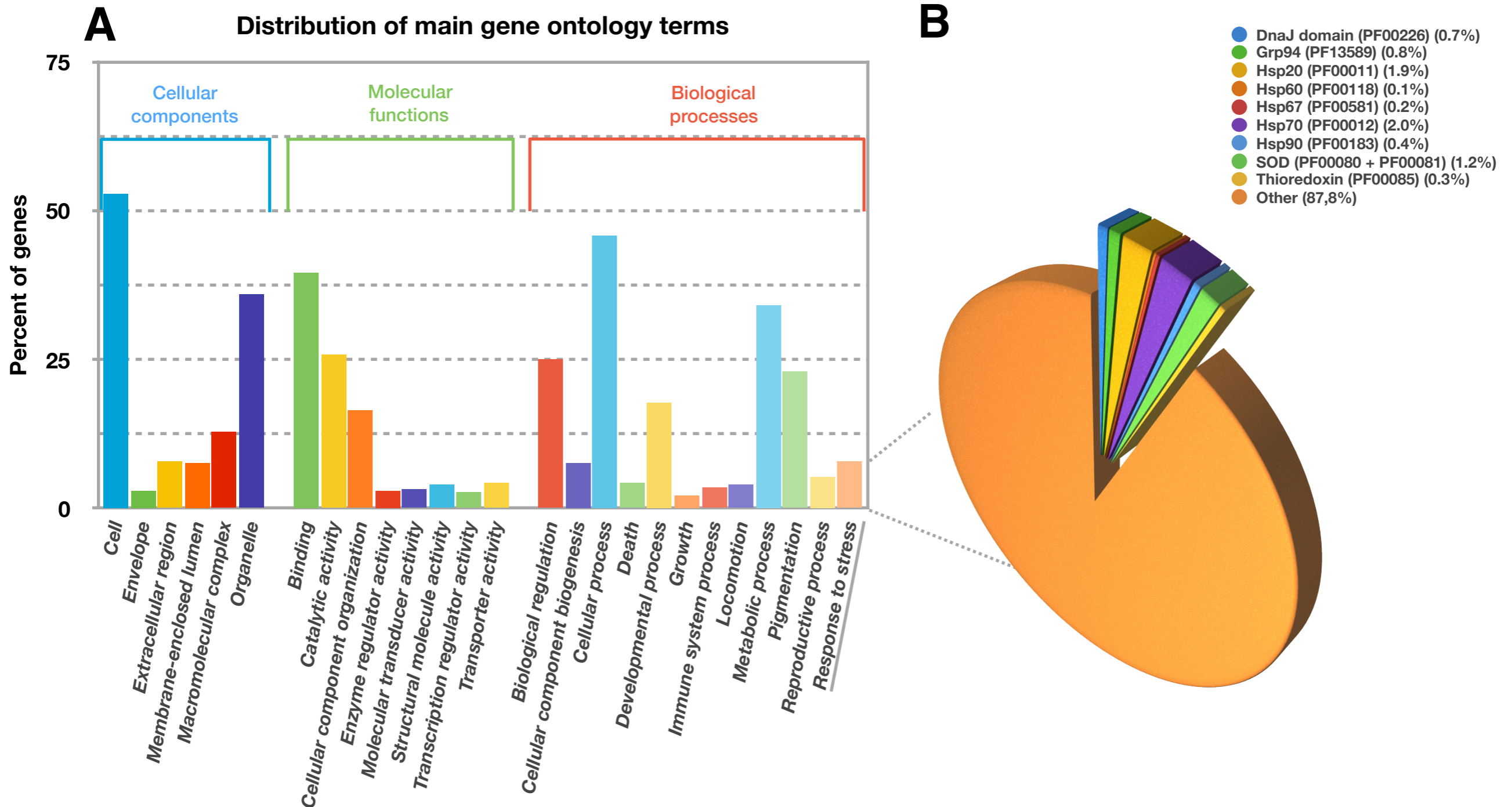


Online Resources 1

Distribution of gene ontology terms of the *T. inermis* transcriptome. (A) The most represented categories were divided in three categories: “Biological processes”, “Molecular functions” and “Cellular components”. (B) Subclassification of “Response to stress” with a special focus on *Hsp* transcripts. Figure was created using Keynote 6.6.1 (Apple Inc.).



Database searching identified 3,636 predicted trans-membrane helices; 3,106 signal peptides and 10,746 of them were associated with GOG/NOG annotations, with 13,166 of them having one or more GO annotation. GO slim analysis putatively annotated 12,881 transcripts; whilst 10,547, 11,432 and 10,660 of them had one or more "Biological Process", "Cellular Component" and "Molecular Function" generic GO slim annotations respectively, with only 146 different GO terms shared between them. Figure A illustrates the major GO terms in each of the three categories. Figure B focuses on the GO terms "response to stress".